Delete the paragraph at page 48, lines 26-29 and insert the following:

C1

The P_1' residue can be changed to introduce either charged amino acid side chains or a structurally rigid, *e.g.*, proline, residue as illustrated in the Table 3, substrate sequences for Hepatitis C viral protease substrate NS3 NS5A/5B of DVVCCSMS (SEQ ID NO:165, normal substrate) and DVVCCPdMS (SEQ ID NO:166, inhibitor). The underlined residues are the P_1 residues.

Delete the paragraph at page 49, lines 14-23 and insert the following:

C2

Approximately 1 microgram of protease indicator, having the formula F^1-Asp-Ala-Ile-Pro-Nle-Ser-Ile-Pro-Cys-F^2 (SEQ ID NO:177) where F^1 is a donor fluorophore (5'-carboxytetramethylrhodamine (5-TMR)) linked to aspartic acid via the alpha amino group and F^2 is an acceptor fluorophore (rhodamine X acetamide (R492)) linked via the sulfhydryl group of the cysteine was dissolved in a buffer consisting of 50 mM sodium phosphate, 1 mM EDTA at pH 8.9. To this solution was added 1 unit of elastase. The solution was analyzed by HPLC before and about 30 minutes after the addition of elastase. The digestion was carried out at 37°C. The HPLC separated components were monitored at a wavelength of 550 nm which allowed detection of both the 5-TMR fluorophore the R492 fluorophore and at 580 nm which allowed detection of the R492 fluorophore.

Delete the paragraph at page 52, lines 13-21 and insert the following:

C3

~~Fluorophores were linked to the amino terminus via the α-amino group of aspartic acid residue (D) and to the ε-amino group of lysine (K). Labeling was accomplished by the displacement of a succinimidyl group linked to 6-TMR or DER. The structure of the peptide, called NorFES-KGY is:~~

~~Fluorophore1-DAIPNleSIPKGY~~
~~|~~
~~Fluorophore2~~

~~(SEQ ID NO: 168)~~

Delete the paragraph at page 55, lines 7-15 and insert the following:

In addition, we have synthesized and derivatized (homodoubly-labeled) PAI-2, CS-1 (a 31 residue long peptide) and two DEVD-like peptides that did not allow the dye-dye dimer formation. The CS-1 peptide shows that in a significantly longer peptide the dye-dye dimer structure can be formed. Note this peptide contains four proline residues in the amino terminal side of the putative cleavage site Ile-Leu bond. There is one proline in the carboxyl domain also. The results from the CS-1 peptide support a potentially larger sequence between the two dyes (fluorophores). Two DEVD-like peptide's amino acid sequences that did not allow the formation of productive H-type dimers are F_1-DEVDGIDPK[F_1]GY (SEQ ID NO: 169) and F_1-PDEVDGIDPK[F_1]GY (SEQ ID NO: 170).

Delete Table 12 at page 55, line 32 through page 56, line 1 and insert the following:

	Structure	Cellular uptake/ magnitude	Uptake checked by	Seq ID NO
1	Fm-K[F1] DAIPNluSIPK[F1]GY	Yes/high	FM	171
2	K[F1] DAIPNluSIPK[F1]GY	Yes/weak	FM	172
3	Fm-DAIPNluSIPK[F1]GY	No/	FM	173
4	Fm-K[F1]DBDEVDGIDPK[F1]GY	Yes/high	FM & FC	174
5	K[F1]DBDEVDGIDPK[F1]GY	Yes/weak	FM	175
6	Fm-K[F1]DBDEVNGIDPK[F1]GY	Yes/high	FM	176
7	K[F1]DBDEVNGIDPK[F1]GY	Yes/weak	FM & H	177
8	Fm-K[F1]DBEVDGIDPK[F1]GY	Yes/high	FM & FC	178
9	K[F1]DYBADGIDPK[F1]GY	Yes/weak	FM	179
10	Fm-K[F1]DBGDEVDGIDGPK[F1]GY	Yes/high	H & FC	180
11	Fm-K[F1]DBJGDEVDGIDGJPK[F1]GY	Yes/high	FC	181
12	Z-K[F1]DBJGDEVDGIDGJPK[F1]GY	Yes/weak	FM	182

13	Fm-K[F1]DYBADGIDPK[F1]GY	Yes/high	FM	183
14	K[F1]DBEVDGIDPK[F1]GY	Yes/weak	FM	184

Delete the paragraph at page 57, lines 10-21 and insert the following:

~~The elastase substrate, Fm-K[F1]DAIPNluSIPK[F1]GY, (SEQ ID NO: 185,~~ where F1 was carboxytetramethylrhodamine, Fm was Fmoc, K[F1] was F1 covalently attached through the epsilon amino group of lysine (K), and Fm-K is the Fmoc group covalently attached at the alpha amino group of the amino-terminal lysine residue) was used with HL-60 cells. Cells were incubated with various concentrations of elastase substrate ranging from 10 nM to 10 μM for 5 minutes to 60 minutes. Then the cells were diluted 5-fold with RPMI 1640 medium containing 5% serum or with phosphate buffered saline. The samples were centrifuged and washed once more with 1 ml of washing solution. After centrifugation and removal of the washing solution, cell pellets were loosened with about 25 ul of medium and these cells were transferred to a glass capillary. Capillary tubes were then placed on a glass microscope slide and examined under a fluorescence microscope using standard rhodamine filters.

Delete the paragraph at page 58, lines 6-23 and insert the following:

~~Control cells without substrate incubation and the sample with the greatest~~ expected fluorescence signals were used to set the instrument detector parameters. For example after 15 minutes incubation of Jurkat cells with substrate compound #11 Fm-CGD2D: Fm-K[F1]DBJGDEVDGIDGJPK[F1]GY (SEQ ID NO:186, where F1 was carboxytetramethylrhodamine; Fm was Fmoc, K[F1] was F1 covalently attached through the epsilon amino group of lysine (K), Nlu was norleucine, B was aminoisobutyric acid, and J was epsilon-aminocaproic acid) an increase of about 10 channels indicating cellular uptake of the substrates was measured. Note substrate #11 was not completely quenched. Hence, a small amount of background fluorescence would be expected from the intact substrate. Signals from the cells that had been activated with 1 ug/ml of ant-Fas antibody, CH11 clone for 1 to 6 hours indicated an increase in peak channel number. As much as a ten-fold increase in fluorescence intensity was observed. When the cells were co-incubated with the CPP32 ~~protease inhibitor ZVAD-fluoromethylketone at 50 μM along with an apoptosis inducing~~

C7 Conclude

agent, *e.g.*, anti-Fas antibody, this observed increase in fluorescence intensity was eliminated. This indicated that the signal from compound 11 was due to the CPP32 protease activity which was inhibitable by ZVAD-FMK. Hence, the observed fluorescence intensity in each cell as determined by flow cytometric analysis served as a direct measure of the intracellular CPP32 protease activity.

Delete the paragraph at page 59, lines 18-27 and insert the following:

C8 ds 9/10

Jurkat cells are normally grown in 10% fetal calf serum containing RPMI 1640, at 37° C in a 5% CO_2 atmosphere. When the serum content was dropped to 4%, the Jurkat cell growth rate not only slowed down but also a significant number of cells died within 36 hours. The cell density used was about 400,000 cell per ml. After 36 hours, control wells contained about 50% dead cells (trypan blue-positive cells), whereas the wells containing 0.1 or 1.0 μM concentration of compound #11 (Table 12) "Fm-CGD2D" or Fm-K[F1]DBJGDEVDGIDGJPK[F1]GY (SEQ ID NO:187) showed only 10% or 8% nonviable cells. Hence, compound #11 which exhibits efficient cellular uptake slowed down apoptosis in these Jurkat cells where it acted as a CPP32 protease inhibitor or a CPP32 activating protease inhibitor.

Delete the paragraph at page 61, line 26 though page 62, line 15 and insert the following:

C9 ds 9/11

The parent compound Fm-DEVD has the following composition: Fmoc-K[F1]DBDEVDGIDPK[F1]GY (SEQ ID NO:188). The bold face underlined letters are the protease recognition sequence consisting of 7 amino acid residues. Compound #10 contains two glycine extensions at both ends of this protease recognition sequence. The central protease recognition domain now is 8 residues long GDEVDGID (SEQ ID NO:**189**), since the glycine residue at the amino terminus is a part of native sequence. The two glycine residues which are inherently more flexible than other amino acids, *e.g.*, alanine, provide less conformational constraint or, conversely, more flexibility than compound 4 (Table 12) and thereby permit greater flexion when combined with Aib or Pro residues. Additional insertion of amino caproic acid at both termini with five methylene groups in addition to the one present in glycine provides further relaxation of the constrained conformation and, thus,

~~greater flexibility for the protease recognition domain, GDEVDGID (SEQ ID NO:189). This~~ progression of flexibility resulted in an increased hydrolysis rate with the CPP32 protease since CPP32 recognizes a more flexible protease recognition domain than does elastase. Support for this statement is that the CPP32 protease cleavage site in the proform of its physiological substrate, poly(ADP-ribose) polymerase, PARP, is located between two well-folded domains. Hence, it is expected that such a protease cleavage site would not be rigidly held or its conformation would be expected to be less defined than the remaining molecule. Hence, in order to provide these structural features to the substrate, introduction of flexible residues such as glycine, epsilon amino caproic acid, beta alanine, and amino butyric acid would be expected to play important roles in regulating the backbone flexibility of the substrate's central protease recognition domain. These additional preferred residues for the conformation determining domain are also expected to provide the needed bend-inducing influence.

C9 Conclude

Delete the paragraph at page 62, lines 23-29 and insert the following:

~~These examples provide a tetrapeptide and a pentapeptide comprising Lys-~~ Asp-Aib-Gly (SEQ ID NO:190) or Lys-Asp-Aib-Ahx-Gly (SEQ ID NO:191) where Ahx is episilon amino caproic acid (*i.e.* NH_2-$(CH_2)_5$-COOH). The fluorophore is attached to episilon amino group of the lysine residue. The carboxyl terminal CDR domain is defined as a tripeptide Gly-Pro-Lys and a tetrapeptide Gly-Ahx-Pro-Lys (SEQ ID NO:192). The hydrolysis rate was increased by 3-fold between compounds 4 (Fm-DEVD: Fm-K[F1]DBDEVDGIDPK[F1]GY, SEQ ID NO: 193) and 10 (Fm-G2D2D: ~~Fm-K[F1]DBGDEVDGIDGPK[F1]GY], SEQ ID NO:194).~~

C10 MS 9/27

Delete the paragraph at page 62, lines 30-34 and insert the following:

~~As illustrated in Figure 5, the hydrolysis rate was further increased by *ca.* 3-~~ fold over the above glycine residue insertion with the amino caproic amino acid (Ahx) addition, compound 11 (Fm-CGD2D: Fm-K[F1]DB Ahx GDEVDGIDG Ahx PK[F1]GY, SEQ ID NO:195). Hence, overall at least a 9-fold increase in substrate hydrolysis rate was ~~accomplished (compounds 4 and 11, Table 12).~~

C11 MS 9/27